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**RAW SEQUENCE LISTING
PATENT APPLICATION US/10/067,477**

DATE: 05/02/2002
TIME: 15:07:19

INPUT SET: S36844.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/067,477DATE: 05/02/2002
TIME: 15:07:20

INPUT SET: S36844.raw

47
48 (vi) CURRENT APPLICATION DATA:
49 (A) APPLICATION NUMBER: 10/067,477
50 (B) FILING DATE:
51 (C) CLASSIFICATION
52
53 (vii) PRIOR APPLICATION DATA:
54
55 (A) APPLICATION NUMBER: 08/796,570
56 (B) FILING DATE: 06-FEB-1997
57
58
59 (A) APPLICATION NUMBER: Japan 8-021562
60 (B) FILING DATE: 2-JUL-1996
61
62 (viii) ATTORNEY/AGENT INFORMATION:
63 (A) NAME: Eisenstein, Ronald I.
64 (B) REGISTRATION NUMBER: 30,628
65 (C) REFERENCE/DOCKET NUMBER: 47147
66
67 (ix) TELECOMMUNICATION INFORMATION:
68 (A) TELEPHONE: 617-523-3400
69 (B) TELEFAX: 617-523-6440
70
71 (2) INFORMATION FOR SEQ ID NO:1:
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 423
74 (B) TYPE: Amino acid
75 (C) TOPOLOGY: Linear
76 (ii) MOLECULE TYPE: Peptide
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
78
79 Met Val Pro His Leu Leu Leu Cys Leu Leu Pro Leu Val Arg Ala
80 1 5 10 15
81 Thr Glu Pro His Glu Gly Arg Ala Asp Glu Gln Ser Ala Glu Ala Ala
82 20 25 30
83 Leu Ala Val Pro Asn Ala Ser His Phe Phe Ser Trp Asn Asn Tyr Thr
84 35 40 45
85 Phe Ser Asp Trp Gln Asn Phe Val Gly Arg Arg Arg Tyr Gly Ala Glu
86 50 55 60
87 Ser Gln Asn Pro Thr Val Lys Ala Leu Leu Ile Val Ala Tyr Ser Phe
88 65 70 75 80
89 Ile Ile Val Phe Ser Leu Phe Gly Asn Val Leu Val Cys His Val Ile
90 85 90 95
91 Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser Leu Phe Ile Val Asn
92 100 105 110
93 Leu Ala Val Ala Asp Ile Met Ile Thr Leu Leu Asn Thr Pro Phe Thr
94 115 120 125
95 Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe Gly Lys Gly Met Cys
96 130 135 140
97 His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu His Val Ser Ala Leu
98 145 150 155 160
99 Thr Leu Thr Ala Ile Ala Val Asp Arg His Gln Val Ile Met His Pro

**RAW SEQUENCE LISTING
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100	165	170	175
101	Leu Lys Pro Arg Ile Ser Ile Thr Lys Gly Val Ile Tyr Ile Ala Val		
102	180	185	190
103	Ile Trp Thr Met Ala Thr Phe Phe Ser Leu Pro His Ala Ile Cys Gln		
104	195	200	205
105	Lys Leu Phe Thr Phe Lys Tyr Ser Glu Asp Ile Val Arg Ser Leu Cys		
106	210	215	220
107	Leu Pro Asp Phe Pro Glu Pro Ala Asp Leu Phe Trp Lys Tyr Leu Asp		
108	225	230	235
109	Leu Ala Thr Phe Ile Leu Leu Tyr Ile Leu Pro Leu Leu Ile Ile Ser		240
110	245	250	255
111	Val Ala Tyr Ala Arg Val Ala Lys Lys Leu Trp Leu Cys Asn Met Ile		
112	260	265	270
113	Gly Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu Arg Arg Lys Lys Lys		
114	275	280	285
115	Lys Thr Ile Lys Met Leu Met Leu Val Val Val Leu Phe Ala Leu Cys		
116	290	295	300
117	Trp Phe Pro Leu Asn Cys Tyr Val Leu Leu Leu Ser Ser Lys Val Ile		
118	305	310	315
119	Arg Thr Asn Asn Ala Leu Tyr Phe Ala Phe His Trp Phe Ala Met Ser		320
120	325	330	335
121	Ser Thr Cys Tyr Asn Pro Phe Ile Tyr Cys Trp Leu Asn Glu Asn Phe		
122	340	345	350
123	Arg Ile Glu Leu Lys Ala Leu Leu Ser Met Cys Gln Arg Pro Pro Lys		
124	355	360	365
125	Pro Gln Glu Asp Arg Pro Pro Ser Pro Val Pro Ser Phe Arg Val Ala		
126	370	375	380
127	Trp Thr Glu Lys Asn Asp Gly Gln Arg Ala Pro Leu Ala Asn Asn Leu		
128	385	390	395
129	Leu Pro Thr Ser Gln Leu Gln Ser Gly Lys Thr Asp Leu Ser Ser Val		400
130	405	410	415
131	Glu Pro Ile Val Thr Met Ser		
132	420		
133			
134	(2) INFORMATION FOR SEQ ID NO:2:		
135	(i) SEQUENCE CHARACTERISTICS:		
136	(A) LENGTH: 1272		
137	(B) TYPE: Nucleic acid		
138	(C) STRANDEDNESS: Double		
139	(C) TOPOLOGY: Linear		
140	(ii) MOLECULE TYPE: cDNA		
141	(xi) FEATURE:		
142	(C) IDENTIFICATION METHOD: S		
143	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		
144			
145	ATGGTCCCTC ACCTCTTGCT GCTCTGTCTC CTCCCCTTGG TGCGAGCCAC CGAGCCCCAC	60	
146	GAGGGCCGGG CCGACGAGCA GAGCGCGGAG GCGGCCCTGG CCGTGCCCAA TGCCTCGCAC	120	
147	TTCTTCTCTT GGAACAACTA CACCTTCTCC GACTGGCAGA ACTTTGTGGG CAGGAGGCAG	180	
148	TACGGCGCTG AGTCCCAGAA CCCCACGGTG AAAGCCCTGC TCATTGTGGC TTACTCCTTC	240	
149	ATCATTGTCT TCTCACTCTT TGGCAACGTC CTGGTCTGTC ATGTCATCTT CAAGAACAG	300	
150	CGAATGCACT CGGCCACCAG CCTCTTCATC GTCAACCTGG CAGTTGCCGA CATAATGATC	360	
151	ACGCTGCTCA ACACCCCCCTT CACTTGGTT CGCTTTGTGA ACAGCACATG GATATTTGGG	420	
152	AAGGGCATGT GCCATGTCAG CCGCTTGCC CAGTACTGCT CACTGCACGT CTCAGCACTG	480	

**RAW SEQUENCE LISTING
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153 ACACTGACAG CCATTGCCGT GGATGCCAC CAGGTCATCA TGCACCCCTT GAAACCCGG 540
154 ATCTCAATCA CAAAGGGTGT CATCTACATC GCTGTCATCT GGACCATGGC TACGTTCTTT 600
155 TCACTCCCAC ATGCTATCTG CCAGAAATTA TTTACCTTCA AATACAGTGA GGACATTGTG 660
156 CGCTCCCTCT GCCTGCCAGA CTTCCCTGAG CCAGCTGACC TCTTCTGGAA GTACCTGGAC 720
157 TTGCCACCT TCATCCTGCT CTACATCCTG CCCCTCCTCA TCATCTCTGT GGCCTACGCT 780
158 CGTGTGGCCA AGAAAATGTG GCTGTGTAAT ATGATTGGCG ATGTGACCAC AGAGCAGTAC 840
159 TTTGCCCTGC GGCGCAAAAAA GAAGAAGACC ATCAAGATGT TGATGCTGGT GTAGTCCTC 900
160 TTTGCCCTCT GCTGGTTCCTC CCTCAACTGC TACGTCCCTCC TCCTGTCCAG CAAGGTCACTC 960
161 CGCACCAACA ATGCCCTCTA CTTTGCCCTC CACTGGTTG CCATGAGCAG CACCTGCTAT 1020
162 AACCCCTCA TATACTGCTG GCTGAACGAG AACTTCAGGA TTGAGCTAAA GGCATTACTG 1080
163 AGCATGTGTC AAAGAACCTCC CAAGCCTCAG GAGGACAGGC CACCCCTCCCC AGTTCCCTCC 1140
164 TTCAGGGTGG CCTGGACAGA GAAGAATGAT GGCCAGAGGG CTCCCTTGCA CAATAACCTC 1200
165 CTGCCACCT CCCAACTCCA GTCTGGGAAG ACAGACCTGT CATCTGTGGA ACCCATTGTG 1260
166 ACGATGAGTT AG 1272
167
168 (2) INFORMATION FOR SEQ ID NO:3:
169   (i) SEQUENCE CHARACTERISTICS:
170     (A) LENGTH: 70
171     (B) TYPE: Amino acid
172     (C) TOPOLOGY: Linear
173   (ii) MOLECULE TYPE: Peptide
174   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
175
176 Val Cys His Val Ile Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser
177      1           5          10          15
178 Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met Ile Thr Leu Leu
179      20          25          30
180 Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe
181      35          40          45
182 Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu
183      50          55          60
184 His Val Ser Ala Leu Thr
185      65          70
186
187 (2) INFORMATION FOR SEQ ID NO:4:
188   (i) SEQUENCE CHARACTERISTICS:
189     (A) LENGTH: 71
190     (B) TYPE: Amino acid
191     (C) TOPOLOGY: Linear
192   (ii) MOLECULE TYPE: Peptide
193   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
194
195 Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile
196      1           5          10          15
197 Leu Leu Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg
198      20          25          30
199 Val Thr Lys Lys Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr
200      35          40          45
201 Glu Gln Tyr Phe Ala Leu Arg Pro Lys Lys Lys Lys Thr Ile Lys Met
202      50          55          60
203 Leu Met Leu Val Val Val Leu
204      65          70
205

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RAW SEQUENCE LISTING
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206 (2) INFORMATION FOR SEQ ID NO:5:
207 (i) SEQUENCE CHARACTERISTICS:
208 (A) LENGTH: 210
209 (B) TYPE: Nucleic acid
210 (C) STRANDEDNESS: Double
211 (C) TOPOLOGY: Linear
212 (ii) MOLECULE TYPE: cDNA
213 (xi) FEATURE:
214 (C) IDENTIFICATION METHOD: S
215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
216
217 GTCTGTCATG TCATCTTCAA GAACCAGCGA ATGCACTCGG CCACCAGCCT CTTCATCGTC 60
218 AACCTGGCAG TTGCCGACAT AATGATCACG CTGCTCAACA CCCCCCTTCAC TTTGGTTCGC 120
219 TTTGTGAACA GCACATGGAT ATTGGGAAG GGCATGTGCC ATGTCAGCCG CTTTGCCCAG 180
220 TACTGCTCAC TGCACGTCTC AGCACTGACA 210
221
222 (2) INFORMATION FOR SEQ ID NO:6:
223 (i) SEQUENCE CHARACTERISTICS:
224 (A) LENGTH: 213
225 (B) TYPE: Nucleic acid
226 (C) STRANDEDNESS: Double
227 (C) TOPOLOGY: Linear
228 (ii) MOLECULE TYPE: cDNA
229 (xi) FEATURE:
230 (C) IDENTIFICATION METHOD: S
231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
232
233 GAGCCAGCTG ACCTCTTCTG GAAGAACCTG GACTTGCCCA CCTTCATCCT GCTCAACATC 60
234 CTGCCCCCTCC TCATCATCTC TGTGCCCTAC GTTCGTGTGA CCAAGAAACT GTGGCTGTGT 120
235 AATATGATTG TCGATGTGAC CACAGAGCAG TACTTTGCCG TGCGGCCAA AAAGAAGAAG 180
236 ACCATCAAGA TGTTGATGCT GGTGGTAGTC CTC 213
237
238 (2) INFORMATION FOR SEQ ID NO:7:
239 (i) SEQUENCE CHARACTERISTICS:
240 (A) LENGTH: 25
241 (B) TYPE: Nucleic acid
242 (C) STRANDEDNESS: Single
243 (C) TOPOLOGY: Linear
244 (ii) MOLECULE TYPE: Other nucleic acid Synthetic
245 DNA
246 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
247
248 CGTGGSCMTS STGGGCAACN YCCTG 25
249
250 (2) INFORMATION FOR SEQ ID NO:8:
251 (i) SEQUENCE CHARACTERISTICS:
252 (A) LENGTH: 27
253 (B) TYPE: Nucleic acid
254 (C) STRANDEDNESS: Single
255 (C) TOPOLOGY: Linear
256 (ii) MOLECULE TYPE: Other nucleic acid Synthetic
257 DNA
258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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**SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/10/067,477**

DATE: 05/02/2002
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INPUT SET: S36844.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Shuji HINUMA
7	Unknown or Misplaced Identifier	(B) STREET: 7-9-1402, Kasuga 1-chome
8	Unknown or Misplaced Identifier	(C) CITY: Tsukuba
9	Unknown or Misplaced Identifier	(D) STATE: Ibaraki
10	Unknown or Misplaced Identifier	(E) COUNTRY: Japan
11	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 305
14	Unknown or Misplaced Identifier	(A) NAME: Junichi SAKAMOTO
15	Unknown or Misplaced Identifier	(B) STREET: 14-30-A103, Kamishinden 1-chome
16	Unknown or Misplaced Identifier	(C) CITY: Toyonaka
17	Unknown or Misplaced Identifier	(D) STATE: Osaka
18	Unknown or Misplaced Identifier	(E) COUNTRY: Japan
19	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 565
22	Unknown or Misplaced Identifier	(A) NAME: Masaki HOSOYA
23	Unknown or Misplaced Identifier	(B) STREET: 711-83, Itaya 1-chome
24	Unknown or Misplaced Identifier	(C) CITY: Tsuchiura
25	Unknown or Misplaced Identifier	(D) STATE: Ibaraki
26	Unknown or Misplaced Identifier	(E) COUNTRY: Japan
27	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 300

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**SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/10/067,477**

DATE: 05/02/2002
TIME: 15:07:21

INPUT SET: S36844.raw

GENERAL INFORMATION More Identifiers Found Than MAX Allowed

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SEQUENCE CORRECTION REPORT
PATENT APPLICATION **US/10/067,477**

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INPUT SET: S36844.raw

Line	Original Text	Corrected Text
51	(C) CLASSIFICATION	(C) CLASSIFICATION:
138	(C) STRANDEDNESS: Double	(C) STRANDEDNESS: Double
141	(xi) FEATURE	(xi) FEATURE:
210	(C) STRANDEDNESS: Double	(C) STRANDEDNESS: Double
213	(xi) FEATURE	(xi) FEATURE:
226	(C) STRANDEDNESS: Double	(C) STRANDEDNESS: Double
229	(xi) FEATURE	(xi) FEATURE: